## SEOUENCE LISTING

<120> POLYPEPTIDES FOR INDUCING A PROTECTIVE IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS <130> 21569Y PCT <150> 60/489,840

<150> 60/520,115 <151> 2003-11-14

<151> 2003-07-24

<110> Merck & Co., Inc.

<160> 107

<170> FastSEQ for Windows Version 4.0

<210> 1 <211> 446 <212> PRT <213> Artificial Sequence

<223> ORF0657n with amino terminus methionine

<400> 1

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Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys 185

Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys 200

170

190

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Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala
Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala
                   230
                                       235
Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn
                                  250
Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys
                               265
Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala
                           280
                                                285
Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp
                       295
                                           300
Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu
                    310
                                        315
Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu
               325
                                    330
Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp
                                345
Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp
        355
                            360
Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys
                        375
                                            380
Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr
                   390
                                        395
Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys
                405
                                    410
Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Asp Asn Ser Ala
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                                425
Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro
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<210> 2 <211> 645 <212> PRT

<213> S. aureus

<400> 2

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Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly 150 155 Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val 165 170 Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly 180 185 Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro 195 200 Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg 215 Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr 230 His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe 245 , 250 Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp 260 265 Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu 280 Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu 295 Lys Leu Lys Ala Glu Tyr Lys Lys Leu Glu Asp Thr Lys Lys Ala 310 315 Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln 325 330 Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val 340 345 Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys 360 His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met 375 380 Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln 395 390 Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile 410 Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys 420 425 Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile 440 Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys 455 460 Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr 470 475 Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln 485 490 Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu 505 Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys 520 Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val 535 540 Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys 550 555 Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys 570

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Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
      580
                              585
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
                         600
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
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                                   620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
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Arg Lys Arg Lys Asn
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Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr
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Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala
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Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala
                       55
Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn
                                       75
Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro
                                   90
Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp
                               105
Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala
                           120
                                              125
Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu
                       135
 Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val
                   150
                                       155
Tyr Glu Gly Asp Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr
                                  170
                165
                                                      175
Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys
           180
                               185
                                                  190
 Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys
                           200
                                               205
 Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala
                       215
                                           220
 Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala
                   230
                                      235
 Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn
                                  250
               245
 Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys
                               265
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Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala

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Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp
                       295
Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu
                   310
                                       315
Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu
               325
                                   330
Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp
                                345
Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp
                           360
                                                365
Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys
                       375
                                            380
Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr
                   390
                                        395
Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys
               405
                                   410
Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala
            420
                               425
Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro
                            440
                                                445
Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys
                        455
Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly
                   470
                                        475
Lys Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser
                485
                                    490
Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala
            500
                                505
Lys Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr
        515
                            520
Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala
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Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys
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Asn Thr Gln Glu Asn Lys Ala Lys Ser
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<210> 4
<211> 570
<212> PRT
<213> Artificial Sequence
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<220>

<223> ORF0657nH with amino terminus methionine-glycine

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Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn 85 90 Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile 100 105 Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr 120 Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro 135 Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu 150 155 Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp 170 Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr 185 Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu 200 Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser 215 Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu 230 235 Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu 245 250 Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys 265 270 Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser 280 285 Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr 295 Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn 310 315 Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met 330 Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr 345 Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys 360 Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly 375 380 Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp 390 395 Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr 405 410 Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser 420 425 430 Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser 440 435 Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn 455 460 Lys Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser 470 475

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Gly Lys Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu
              485
                            490
Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val
                               505
Ala Lys Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln
                           520
                                              525
Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys
                       535
                                       540
Ala Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn
                550
                                       555
Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
<210> 5
<211> 447
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<213> Artificial Sequence
<223> ORF0657nH with amino terminus methionine-glycine
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Thr Glu Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu
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Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu
                            40
Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys
Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn
                    70
Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn
                                    90
Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile
                                105
Asp Phe Glu Met Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr
                            120
Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro
                        135
                                            140
Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu
                    150
                                        155
Val Tyr Glu Gly Asp Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp
                165
                                    170
                                                        175
Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr
            180
                                185
Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu
                            200
                                                205
Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser
                        215
                                            220
Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu
                    230
                                        235
Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu
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                                    250
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Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys
                 265
Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser
                          280
                                              285
Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr
                      295
                                          300
Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn
                  310
                                      315
Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met
               325
                                  330
Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr
           340
                               345
Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys
                           360
Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly
                       375
Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp
                   390
                                       395
Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr
               405
                                   410
Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser
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Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro
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Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
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Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys
                            40
Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys
                        55
Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro
                                        75
Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
                                    90
Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
                                105
Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr
                           120
                                               125
Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile
                        135
                                           140
 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln
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150

Dho	<b>6</b> 0	7 ~~	Tura	Dha	C1	1707	m	<b>~</b> 3	<b>~</b> 1	3	<b>7</b> –			_	
			Lys	165					170					175	
Lys	Leu	Val	Ser 180	Tyr	Asp	Thr	Val	Lys 185	Asp	Tyr	Ala	Tyr	Ile 190	Arg	Phe
Ser	Val	Ser 195	Asn	Gly	Thr	ГЛS	Ala 200	Val	Lys	Ile	Val	Ser 205	Ser	Thr	His
Phe	Asn 210	Asn	Lys	Glu	Glu	Lys 215	Tyr	Asp	Tyr	Thr	Leu 220	Met	Glu	Phe	Ala
Gln 225	Pro	Ile	Tyr	Asn	Ser 230	Ala	Asp	Lys	Phe	Lys 235		Glu	Glu	Asp	Tyr 240
	Ala	Glu	Lys	Leu 245		Ala	Pro	Tyr	Lys 250		Ala	Lys	Thr	Leu 255	
Arg	Gln	Val	Tyr 260		Leu	Asn	Lys	Ile 265		Asp	Lys	Leu	Pro 270		Lys
Leu	Lys	Ala 275	Glu	Tyr	Lys	Lys	Lys 280	_	Glu	Glu	Thr	Lys 285		Ala	Leu
Asp	Glu 290		Val	Lys	Ser	Ala 295		Thr	Glu	Phe	Gln 300		Val	Gln	Pro
Thr 305	Asn	Glu	Lys	Met	Thr 310		Leu	Gln	Asp	Thr 315		Tyr	Val	Val	Tyr 320
Glu	Ser	Val	Glu	Asn 325		Glu	Ser	Met	Met 330		Ala	Phe	Val	Lys 335	
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly 345	Lys	Lys	Tyr	Met	Val 350		Glu
Thr	Thr	Asn 355	Asp	Asp	Tyr	Trp	Lys 360	Asp	Phe	Met	Val	Glu 365		Gln	Arg
Val	Arg 370	Thr	Ile	Ser	Lys	Asp 375		Lys	Asn	Asn	Thr 380	Arg	Thr	Ile	Ile
Phe 385	Pro	Tyr	Val	Glu	Gly 390		Thr	Leu	Tyr	Asp 395		Ile	Val	Lys	Val 400
His	Val	Lys	Thr	Ile 405		Tyr	Asp	Gly	Gln 410		His	Val	Arg	Ile 415	Val
Asp	Lys	Glu	Ala 420		Thr	Lys	Ala	Asn 425	Ala	Asp	Lys	Thr	Asn 430	Lys	Lys
Glu	Gln	Gln 435	Asp	Asn	Ser	Ala	Lys 440		Glu	Thr	Thr	Pro 445		Met	Pro
Ser	Lys 450		Thr	Thr	Pro	Pro 455		Glu	Lys	Glu	Ser		Lys	Gln	Asp
Ser 465		Lys	Asp	Asp	Asn 470		Gln	Ser	Pro	Ser 475		Glu	Lys	Glu	Asn 480
Asp	Ala	Ser	Ser	Glu 485		Gly	Lys	Asp	Lys 490		Pro	Val	Thr	Lys 495	Pro
Ala	Lys	Ala	Glu 500		Glu	Ser	Ser	Ser 505		Thr	Pro	Thr	Lys 510		Val
Ser	Thr	Thr 515		Asn	val	. Ala	Lys 520		Thr	Thr	Ala	Ser 525		Glu	Thr
Thr	Lys 530		Val	. Val	. Gln	Thr 535		Ala	Gly	Ser	Ser 540		Ala	Lys	Asp
Ser 545		Pro	Lev	Glr	Lys 550		Asn	Ile	Lys	Asn 555		Asn	Asp	Gly	His 560
Thr	Gln	Ser	Glr	Asr 565		Lys	s Asn	Thr	Glr 570		Asn	Lys	: Ala	Lys 575	Ser

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Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp 395 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala 405 410 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys 420 425 430 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val 440 445 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln 455 460 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys 470 475 Gly Val Thr Leu Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser 485 490 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys 500 505 Pro Thr Thr Gly Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser 515 520 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn 535 Ile Lys His Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn 550 555 Thr Gln Glu Asn Lys Ala Lys Ser 565 <210> 8 <211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 8

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Glu	Gly	qaA	Lys	Lvs	Leu	Pro	Ile	Lvs	Leu	Val	Ser	Tvr	azA	Thr	Val
				165					170					175	
rys	Asp	Туr	180	Tyr	Ile	Arg	Phe	Ser 185	Val	Ser	Asn	СІУ	Thr 190	Lys	Ala
		195					His 200					205		_	_
Asp	Tyr 210	Thr	Leu	Met	Glu	Phe 215	Ala	Gln	Pro	Ile	Tyr 220	Asn	Ser	Ala	Asp
Lys 225	Phe	Lys	Thr	Glu	Glu 230	Asp	Tyr	Lys	Ala	Glu 235	Lys	Leu	Leu	Ala	Pro 240
Tyr	Lys	Lys	Ala	Lys 245	Thr	Leu	Glu	Arg	Gln 250	Val	Tyr	Glu	Leu	Asn 255	Lys
Ile	Gln	Asp	Lys 260	Leu	Pro	Glu	Lys	Leu 265	Lys	Ala	Glu	Tyr	Lys 270	Lys	Lys
Leu	Glu	Asp 275	Thr	Lys	Lys	Ala	Leu 280	Asp	Glu	Gln	Val	Lys 285	Ser	Ala	Ile
Thr	Glu 290	Phe	Gln	Asn	Val	Gln 295	Pro	Thr	Asn	Glu	Lys 300	Met	Thr	Asp	Leu
305					310		Tyr			315					320
Met	Met	Asp	Thr	Phe 325	Val	Lys	His	Pro	Ile 330		Thr	Gly	Met	Leu 335	Asn
			340				Glu	345					350	_	_
Asp	Phe	Met 355		Glu	Gly	Gln	Arg 360	Val	Arg	Thr	Ile	Ser 365	Lys	Asp	Ala
Lys	Asn 370		Thr	Arg	Thr	Ile 375	Ile	Phe	Pro	Tyr	Val 380	Glu	Gly	Lys	Thr
Leu 385		Asp	Ala	Ile	Val 390		Val	His	Val	Lys 395		Ile	Asp	Tyr	Asp 400
Gly	Gln	Tyr	His	Val 405		Ile	Val	Asp	Lys 410		Ala	Phe	Thr	Lys 415	Ala
Asn	Thr	Asp	Lys 420		Asn	Lys	Lys	Glu 425		Gln	Asp	Asn	Ser 430	Ala	Lys
Lys	Glu	Ala 435		Pro	Ala	Thr	Pro 440		. Lys	Pro	Thr	Pro 445		Pro	Val
Glu	Lys 450		Ser	Gln	Lys	Gln 455		Ser	Gln	Lys	Asp 460		Asn	Lys	Gln
Leu 465		Ser	· Val	. Glu	Lys 470		. Asn	Asp	Ala	Ser 475		Glu	Ser	Gly	Lys 480
Asp	Lys	Thi	Pro	Ala 485		Lys	Pro	Thr	Lys 490		Glu	Val	. Glu	Ser 495	Ser
Ser	Thr	Thi	Pro 500		Lys	val	. Val	. Ser 509		Thr	Gln	Asn	Val 510		Lys
Pro	Thr	Th:		a Sei	Ser	Lys	520		: Lys	s Asp	Val	. Val		Thr	Ser
Ala	Gl <sub>3</sub> 530		r Sei	Gli	ı Ala	Lys 535	_	Se:	Ala	a Pro	Let 540	Glr		Ala	Asn
Ile 545		s Ası	n Thi	Ası	n Asp 550		/ His	Thi	c Glı	n Sei 559		a Asr	n Asr	Lys	Asn 560
Thi	Glr	ı Glı	u Ası	1 Ly:		a Ly:	s Sei	<u> </u>							

<210> 9 <211> 568

<212> PRT <213> Artificial Sequence <220> <223> ORF0657nH <400> 9 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala 90 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe 105 Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser 120 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile 135 140 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr 150 155 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val 165 170 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala 185 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr 200 205 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp 215 220 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro 230 235 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys 245 250 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys 265 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile 280 285 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu 295 300 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser 310 315 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn 325 330 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys 340 345 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala 360 365 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr 370 375 380

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp 390 395 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala 405 410 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Asp Asn Ser Ala Lys 420 425 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val 435 440 445 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln 455 460 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys 470 475 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser 485 490 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys 500 505 510 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser 515 520 525 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn 535 540 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn 550 · 555 Thr Gln Glu Asn Lys Ala Lys Ser 565

<210> 10

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 10

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu 10 Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro 40 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala 90 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe 105 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser 120 125 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile 135 140 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr 155

Glu	Clv	λcn	Tue	Tvc	Lau	Dro	T1.	T	T 011	1701	C 0 30	m	3	<b>60</b> 1	**- 1
			Lys	165					170					175	
Lys	Asp	Tyr	Ala 180	Tyr	Ile	Arg	Phe	Ser 185	Val	Ser	Asn	Gly	Thr 190	Lys	Ala
Val	Lys	Ile 195	Val	Ser	Ser	Thr	His 200	Phe	Asn	Asn	Lys	Glu 205	Glu	Lys	Tyr
Asp	Tyr 210	Thr	Leu	Met	Glu	Phe 215		Gln	Pro	Ile	Tyr 220		Ser	Ala	Asp
Lys 225		Lys	Thr	Glu	Glu 230		Tyr	Lys	Ala	Glu 235		Leu	Leu	Ala	Pro 240
	Lys	Lys	Ala	Lys 245		Leu	Glu	Arg	Gln 250		Tyr	Glu	Leu	Asn 255	
Ile	Gln	Asp	Lys 260		Pro	Glu	Lys	Leu 265		Ala	Glu	Tyr			Lys
Leu	Glu	Asp 275	Thr	Lys	Lys	Ala	Leu 280		Glu	Gln	Val		270 Ser	Ala	Ile
Thr	Glu 290		Gln	Lys	Val	Gln 295		Thr	Asn	Glu		285 Met	Thr	Asp	Leu
Gln 305		Thr	Lys	Tyr	Val 310		Tyr	Glu	Ser		300 Glu	Asn	Asn	Glu	
	Met	Asp	Thr	Phe		Lys	His	Pro		315 Lys	Thr	Gly	Met		320 Asn
Gly	Lys	Lys	Tyr		Val	Met	Glu		330 Thr	Asn	Asp	Asp		335 Trp	Lys
Asp	Phe		340 Val	Glu	Gly	Gln		345 Val	Arg	Thr	Ile		350 Lys	Asp	Ala
Lys			Thr	Arg	Thr		360 Ile	Phe	Pro	Tyr		365 Glu	Gly	Lys	Thr
			Ala	Ile		375 Lys	Val	His	Val		380 Thr	Ile	Asp	Tyr	Asp
385		/D		17-7	390	<b>-</b> 1-	*** 1	•	<b>.</b>	395		-1	_,	_	400
			His -	405					410					415	
			420					425					430		_
		435					440					445			
	450					455					460				Gln
Leu 465		Ser	· Val	Glu	Lys 470		Asn	Asp	Ala	Ser 475		Glu	Ser	Gly	Lys 480
Asp	Lys	Thr	Pro		Thr					Gly				Ser 495	
Ser	Thr	Thr	Pro 500		Lys	Val	Val	Ser 505		Thr	Gln	Asn	Val 510		Lys
Pro	Thr	Thr 515		Ser	Ser	Lys	Thr 520		Lys	asp	Val	Val 525		Thr	Ser
Ala	Gly 530		Ser	Glu	Ala	Lys 535	Asp		Ala	Pro	Leu 540	Gln		Ala	Asn
Ile 545	: Lys		Thr	Asr	Asp 550	Gly		Thr	Glr	Ser 555	Gln		Asn	Lys	Asn 560
		Glu	ı Asn	Lys 565	a Ala		Ser	•		200					

<210> 11 <211> 565

<212> PRT <213> Artificial Sequence <220> <223> ORF0657nH <400> 11 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu 10 Ala Val Ala Ser Pro Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys 20 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro 40 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr 55 Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile 70 Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp 85 90 Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys 105 Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys 120 Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly 135 Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp 150 155 Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr 170 Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile 185 Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr 200 Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys 215 220 Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys 230 235 Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp 245 250 Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Leu Glu Asp 265 Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe 280 Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr 295 300 Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp 310 315 Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys 330 325 Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met 345 Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn 360 Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp 370

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Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr
385
                  390
                                      395
His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp
               405
Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala
           420
                               425
Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu
                           440
Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser
                       455
                                          460
Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr
                   470
                                       475
Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr
                                   490
Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr
                               505
Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser
                           520
                                               525
Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn
                       535
                                          540
Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu
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Asn Lys Ala Lys Ser
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<210> 12

<211> 566

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 12

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu 10 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro 40 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro 55 Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr 70 75 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala 85 90 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe 100 105 Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser 120 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile 135 140 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr 150 155

Glu	Gly	Asp	Lys	Lys 165	Leu	Pro	Ile	Lys	Leu 170	Val	Ser	Tyr	Asp	Thr 175	Val
Lys	Asp	Tyr	Ala 180	Tyr	Ile	Arg	Phe	Ser 185		Ser	Asn	Gly	Thr 190	Lys	Ala
Val	Lys	Ile 195	Val	Ser	Ser	Thr	His 200	Phe	Asn	Asn	Lys	Glu 205	Glu	Lys	Tyr
	210					215				Ile	220				
225					230					Glu 235					240
				245					250	Val				255	
			260					265	_	Ala		-	270		
		275					280			Gln		285			
	290					295				Glu	300				
305	Asp	Thr	Lys	Tyr	Val 310	Val	Tyr	Glu	Ser	Val 315	Glu	Asn	Asn	Glu	Ser 320
Met	Met	Asp	Thr	Phe 325		Lys	His	Pro	11e 330	Lys	Thr	Gly	Met	Leu 335	Asn
			340					345		Asn			350		
_		355			_		360		_	Thr		365	_	_	
	370					375				Tyr	380				
385	_	_			390	-				Lys 395			_	_	400
				405	•			_	410					415	
			420	)				425		Gln			430		_
гÀа	GIU	435		Pro	) Ala	Thr	440		. Lys	Pro	Thr	445		Pro	Val
	450	)				455	;				460				Gln
Leu 465		Sei	· Val	Glu	1 Lys 470		ı Asn	Asp	) Ala	Ser 475		Glu	Ser	Gly	Lys 480
Asp	Lys	Thi	e Pro	Ala 485		Lys	Pro	Thr	Lys 490	_	Glu	Val	. Glu	Ser 495	Ser
Thr	Thi	Pro	Th: 500		s Val	l Val	l Ser	Thr 505		Gln	Asn	Val	. Ala		Pro
Thr	Ala	Se: 51!		r Lys	3 Thr	Thi	520		Val	l Val	. Glr	Th: 525		Ala	Gly
	530	)				535	5				540	)			E Lys
545	5				550	)	r Gli	n Sei	r Glı	n Asr 555		ı Lys	s Ası	1 Thi	Gln 560
Glı	ı Ası	n Ly:	s Ala	a Ly:	s Sei 5	r									

<sup>&</sup>lt;210> 13 <211> 568

<212> PRT <213> Artificial Sequence <220> <223> ORF0657nH <400> 13 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu 10 Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro 40 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala 85 90 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe 105 Glu Met Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser 120 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile 135 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr 150 155 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val 165 170 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala 185 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr 195 200 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp 215 220 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro 230 235 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys 250 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys 265 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile 280 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu 295 300 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser 310 315 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn 330 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys 345 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala 360 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr 375

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp 390 395 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala 410 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Asp Asn Ser Ala Lys 420 425 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val 440 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln 455 460 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys 470 475 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Lys Val Glu Ser Ser 485 490 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys 505 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser 520 525 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn 535 540 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn 550 555 Thr Gln Glu Asn Lys Ala Lys Ser 565

<210> 14

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 14

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu 5 10 Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro 40 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro 55 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr 75 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Glu 90 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe 105 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser 120 125 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile 135 140 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr 155

Glu	Gly	Asp	Lys	Lys 165	Leu	Pro	Ile	Lys	Leu 170	Ala	Ser	Tyr	Asp	Thr 175	Val
Lys	Asp	Tyr	Ala 180	Tyr	Ile	Arg	Phe	Ser 185	Ile	Ser	Asn	Gly	Thr 190	Lys	Ala
Val	Lys	Ile 195	Val	Ser	Ser	Thr	His 200	Phe	Asn	Asn	Lys	Glu 205	Glu	Lys	Tyr
Asp	Tyr 210	Thr	Leu	Met	Glu	Phe 215	Ala	Gln	Pro	Ile	Tyr 220	Asn	Ser	Ala	Asp
Lys 225	Phe	Lys	Thr	Glu	Glu 230	qaA	Tyr	Lys	Ala	Glu 235	Lys	Leu	Leu	Ala	Pro 240
Tyr	Lys	Lys	Ala	Lys 245	Thr	Leu	Glu	Arg	Gln 250	Val	Tyr	Glu	Leu	Asn 255	Lys
Ile	Gln	Asp	Lys 260	Leu	Pro	Glu	Lys	Leu 265	Lys	Ala	Glu	Tyr	Lys 270		Lys
Leu	Glu	Asp 275	Thr	Lys	Lys	Ala	Leu 280	Asp	Glu	Gln	Val	Lys 285	Ser	Ala	Ile
Thr	Glu 290	Phe	Gln	Asn	Val	Gln 295	Pro	Thr	Asn	Glu	Lys 300	Met	Thr	Asp	Leu
Gln 305	Asp	Thr	Lys	Tyr	Val 310	Val	Tyr	Glu	Ser	Val 315	Glu	Asn	Asn	Glu	Ser 320
Met	Met	Asp	Thr	Phe 325	Val	Lys	His	Pro	Ile 330	Lys	Thr	Gly	Met	Leu 335	Asn
Gly	Lys	Lys	Tyr 340	Met	Val	Met	Glu	Thr 345	Thr	Asn	Asp	Asp	Tyr 350	Trp	Lys
Asp	Phe	Met 355		Glu	Gly	Gln	Arg 360	Val	Arg	Thr	Ile	Ser 365	Lys	Asp	Ala
Lys	Asn 370		Thr	Arg	Thr	I1e 375	Ile	Phe	Pro	Tyr	Val 380	Glu	Gly	Lys	Thr
Leu 385	Tyr	Asp	Ala	Ile	Val 390	Lys	Val	His	Val	Lys 395	Thr	Ile	Asp	Tyr	Asp 400
Gly	Gln	Tyr	His	Val 405		Ile	Val	Asp	Lys 410	Glu	Ala	Phe	Thr	Lys 415	Ala
Asn	Thr	Asp	Lys 420	Ser	Asn	Lys	Lys	Glu 425		Gln	Asp	Asn	Ser 430	Ala	Lys
Lys	Glu	Ala 435		Pro	Ala	Thr	Pro 440		Lys	Pro	Thr	Pro 445	Ser	Pro	Val
Glu	Lys 450		Ser	Gln	Lys	Gln 455		Ser	Gln	Lys	Asp 460		Asn	Lys	Gln
Leu 465		Ser	Val	Glu	Lys 470		Asn	Asp	Ala	Ser 475		Glu	Ser	Gly	Lys 480
				485					490	Gly				495	
Ser	Thr	Thr	Pro 500		Lys	Val	Val	Ser 505		Thr	Gln	Asn	Val 510		Lys
Pro	Thr	Thr 515		Ser	Ser	Lys	Thr 520		Lys	Asp	Val	Val 525		Thr	Ser
Ala	Gly 530		Ser	Glu	Ala	Lys 535		Ser	Ala	Pro	Leu 540		Lys	Ala	Asn
Il∈ 545	Lys	Asn	Thr	Asn	Asp 550		His	Thr	Gln	Ser 555		Asn	Asn	Lys	Asn 560
Thr	Gln	Glu	a Asn	Lys 565		Lys	Ser	•							

<210> 15 <211> 564

<212> PRT <213> Artificial Sequence <220> <223> ORF0657nH <400> 15 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro 40 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys 105 Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys 120 125 Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly 135 140 Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp 150 155 Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr 170 Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile 185 Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr 200 Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys 215 220 Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys 230 235 Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp 250 Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Leu Glu Asp 265 Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe 280 Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr 295 300 Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp 310 315 Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys 330 325 Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met 340 345 Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn 360 Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp 370

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Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr
                                      395
His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp
                                   410
Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala
                               425
Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu
                           440
Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser
                       455
Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr
                  470
                                       475
Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr
               485
                                   490
Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Ala
                               505
Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser Ser
                           520
Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr
                      535
Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn
                   550
                                       555
Lys Ala Lys Ser
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<210> 16

<211> 565

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 16

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro 40 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr 55 Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp 85 Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys 100 105 Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys 120 125 Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly 135 140 Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp 150 155

Lys	Lys	Leu	Pro	Ile 165	Lys	Leu	Val	Ser	Tyr 170	Asp	Thr	Val	Lys	Asp 175	Tyr
Ala	Tyr	Ile	Arg 180		Ser	Val	Ser	Asn 185		Thr	Lys	Ala	Val 190		Ile
Val	Ser	Ser 195	Thr	His	Phe	Asn	Asn 200	Lys	Glu	Glu	Lys	Tyr 205	Asp	Tyr	Thr
	210					215				Ser	220				
225					230					Leu 235					240
				245					250	Leu				255	_
			260					265		Lys			270		
		275					280			Ser		285			
	290					295				Thr Asn	300			_	
305					310					315					320
				325					330					335	
			340					345		Tyr			350		
		355					360			Lys		365			
	370					375				Gly	380				
385					390					Asp 395					400
				405					410					415	_
			420					425		Ser			430		
		435					440					445		_	Glu
	450	ļ.				455				Asn	460				
465	•				470	1				475				_	Thr 480
Pro	Ala	Thr	. Lys	Pro 485		Lys	Gly	Glu	Val 490		Ser	Ser	Ser	Thr 495	Thr
			500	)				505	,				510	)	Thr
Ala	Ser	Ser 515		Thr	Thr	Lys	Asp 520		. Val	l Gln	Thr	Ser 525		Gly	Ser
	530	)				535	5				540	)			Asn
545	5				550		ser	Gln	Asr	n Asn 555		s Asr	Thr	Gln	Glu 560
Asr	ı Lys	s Ala	a Lys	569	_										

<210> 17 <211> 568

<212> PRT <213> Artificial Sequence <220> <223> ORF0657nH <400> 17 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Leu Ala Ser Pro Thr Thr Thr Glu Lys Ala Pro Glu Thr Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro 40 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro 55 Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr 70 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala 85 90 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe 105 Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser 120 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile 135 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr 150 155 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val 165 170 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala 185 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr 195 200 205 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp 215 220 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro 230 235 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys 245 250 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys 265 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile 280 285 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu 295 300 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser 310 315 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn 330 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys 345 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala 360 Ile Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr 375

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Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
                           395
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                                  410
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
          420
                              425
                                                430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                          440
                                             445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                     455
                                         460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
                  470
                                      475
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
               485
                                  490
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
           500
                               505
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
 515
                           520
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
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Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
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Thr Gln Glu Asn Lys Ala Lys Ser
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<210> 18

<211> 565

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

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Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr
         165 170
Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile
         180
                        185
Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr
             200
Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys
                    215
                                    220
Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys
               230
                                 235
Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp
             245
                              250
Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Leu Glu Asp
                           265
Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe
                       280
Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr
                    295
                           300
Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp
                 310
                                 315
Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys
                        330
             325
Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met
                          345 350
Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn
                       360
Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp
                    375
                                      380
Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr
                390
                                  395
His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp
             405
                              410
Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala
          420
                           425
                                            430
Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu
                        440
                                         445
Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Pro Leu Pro Ser
                    455
                                     460
Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr
                470
                                  475
Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr
             485
                              490
Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr
                          505
Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser
      515 520
Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn
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Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu
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Asn Lys Ala Lys Ser
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<210> 19 <211> 568

<212> PRT <213> Artificial Sequence <220> <223> ORF0657nH Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro 40 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro 55 Lys Glu Thr Lys Ala Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr 70 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala 85 90 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe 100 105 Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser 120 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile 135 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr 150 155 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val 170 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala 185 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr 200 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp 215 220 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro 230 235 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys 250 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys 265 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile 280 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu 295 300 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser 310 315 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn 325 330 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys 340 345 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala 360 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr 375

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Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
       390
                         395
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                                 410
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Asp Asn Ser Ala Lys
                             425
Arg Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                         440
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                     455
                                        460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
                 470 . 475
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
              485
                                490
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                             505
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                         520
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
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                             540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
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                                 555
Thr Gln Glu Asn Lys Ala Lys Ser
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Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
                          40
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
Lys Glu Thr Lys Ala Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr
                  70
                                     75
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
               85
                                  90
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
                              105
Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser
                          120
                                            125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
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140

155

135

Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr

Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
Lvs	Asp	Tvr	Ala	165 Tvr	Ile	Ara	Phe	Ser	170 Val	Ser	Asn	Glv	Thr	175 Lvs	Ala
			180					185					190		
		195	Val				200				_	205		_	-
	210		Leu			215					220				
Lys 225	Phe	Lys	Thr	Glu	Glu 230	Asp	Tyr	Lys	Ala	Glu 235	Lys	Leu	Leu	Ala	Pro 240
Tyr	Lys	Lys	Ala	Lys 245	Thr	Leu	Glu	Arg	Gln 250	Val	Tyr	Glu	Leu	Asn 255	Lys
Ile	Gln	Asp	Lys 260	Leu	Pro	Glu	Lys	Leu 265	Lys	Ala	Glu	Tyr	Lys 270	Lys	Lys
Leu	Glu	Asp 275	Thr	Lys	Lys	Ala	Leu 280	Asp	Glu	Gln	Val	Lys 285	Ser	Ala	Ile
Thr	Glu 290	Phe	Gln	Asn	Val	Gln 295	Pro	Thr	Asn	Glu	Lys 300	Met	Thr	Asp	Leu
Gln 305	Asp	Thr	Lys	Tyr	Val 310	Val	Tyr	Glu	Ser	Val 315	Glu	Asn	Asn	Glu	Ser 320
Met	Met	Asp	Thr	Phe 325	Val	Lys	His	Pro	Ile 330		Thr	Gly	Met	Leu 335	Asn
Gly	Lys	Lys	Tyr 340		Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr 350	Trp	Lys
Asp	Phe	Met 355	Val	Glu	Gly	Gln	Arg 360	Val	Arg	Thr	Ile	Ser 365	Lys	Asp	Ala
Lys	Asn 370	Asn	Thr	Arg	Thr	Ile 375	Ile	Phe	Pro	Tyr	Val 380	Glu	Gly	Lys	Thr
Leu 385		Asp	Ala	Ile	Val 390	Lys	Val	His	Val	Lys 395		Ile	Asp	Tyr	Asp 400
Gly	Gln	Tyr	His	Val 405		Ile	Val	Asp	Lys 410		Ala	Phe	Thr	Lys 415	
Asn	Thr	Asp	Lys 420		Asn	Lys	Lys	Glu 425		Gln	Asp	Asn	Ser		Lys
Lys	Glu	Ala 435	Thr	Pro	Ala	Thr	Pro 440		Lys	Pro	Thr	Pro 445		Pro	Val
Glu	Lys 450		Ser	Gln	Lys	Gln 455		Ser	Gln	Lys	Asp 460		Asn	Lys	Gln
Leu 465		Ser	Val	Glu	Lys 470		Asn	Asp	Ala	Ser 475		Glu	Ser	Gly	Lys 480
Asp	Lys	Thr	Pro	Ala 485		Lys	Pro			Gly				Ser 495	Ser
Ser	Thr	Thr	Pro 500		. Lys	Val	Val	Ser 505		Thr	Gln	Asn	Val 510		Lys
Pro	Thr	Thr. 515		Ser	Ser	Lys	Thr 520		Lys	asp	Val	Val 525	Gln		Ser
Ala	Gly 530	ser Ser		Glu	a Ala	Lys 535	Asp		Ala	a Pro	Leu 540	Gln		. Ala	Asn
Ile 545	Lys		ı Thr	Asr	Asp 550	Gly		Thr	Glr	ser 555	Glr		a Asn	Lys	Asn 560
		Glu	ı Asr	1 Lys 565	. Ala		Ser	•							

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<212> PRT <213> Artificial Sequence <220> <223> ORF0657nH <400> 21 Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala 25 Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys 40 Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys 55 Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro 75 Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu 90 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala 105 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr 120 125 Gln Gln Phe Tyr His Tyr Ala Gly Ser Val Lys Pro Ala Arg Val Ile 135 140 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln 150 155 Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile 17Ò 165 Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe 185 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His 200 205 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala 215 220 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr 230 235 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu 245 250 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys 265 Leu Lys Ala Glu Tyr Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu 280 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro 295 300 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr 310 315 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His 325 330 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu 340 345 Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg 360 Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile

375

370

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Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val
                 390
                          395
His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val
              405
                                  410
Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys
                             425
Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro
                         440
                                            445
Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp
                      455
                                         460
Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Gly Val Glu Lys Glu Asn
                 470
                                 475
Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro
              485
                                 490
Ala Lys Ala Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val
                              505
Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr
                         520
Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp
                     535
Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His
545 550
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Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
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<210> 22

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 22

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Phe	Trp	Arg	Lys	Phe 165	Glu	Val	Tyr	Glu	Gly 170	Asp	Lys	Lys	Leu	Pro 175	Ile
Lys	Leu	Va1	Ser 180		Asp	Thr	Val	Lys 185		Tyr	Ala	Tyr	Ile 190		Phe
Ser	Val	Ser 195	Asn	Gly	Thr	Lys	Ala 200	Val	Гуз	Ile	Val	Ser 205	Ser	Thr	His
Phe	Asn 210	Asn	Lys	Glu	Glu	Lys 215	Tyr	Asp	Tyr	Thr	Leu 220	Met	Glu	Phe	Ala
Gln 225	Pro	Ile	Tyr	Asn	Ser 230	Ala	Asp	Lys	Phe	Lys 235	Thr	Glu	Glu	Asp	Tyr 240
Lys				245			Pro		250					255	
Arg			260				Lys	265					270		
		275					Lys 280					285			
	290					295	Ile				300				
305					310		Leu			315					320
				325			Ser		330					335	
			340				Asn	345					350		
		355					Lys 360					365	_		_
	370					375	Ala				380				
385					390		Thr			395					400
				405			Asp		410					415	
			420				Ala	425					430		
		435	ı				Lys 440					445			
	450					455					460				Asp
465					470					475			_		Asn 480
				485	j				490	ı				495	
			500					505					510		Val
		515	•				520					525			Thr
	530	)				535	<b>;</b>				540	l			Asp
545	,				550	)				555	•			_	His 560
Thr	Gln	ı Ser	Glr	Asr 565		Lys	s Asn	Thr	570		ı Asn	Lys	ala	Lys 575	Ser

<210> 23 <211> 568

<212> PRT <213> Artificial Sequence <220> <223> ORF0657nH <400> 23 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu 10 Ala Val Ala Ser Pro Ser Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro 40 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro 55 Lys Glu Thr Lys Glu Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala 90 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe 105 Glu Met Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser 120 125 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile 135 140 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr 150 155 Glu Gly Asn Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val 165 170 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala 185 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr 200 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Gly 215 220 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ser Pro 230 235 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys 245 250 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys 260 265 Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile 280 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu 295 300 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser 310 315 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn 325 330 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys 340 345 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala 360 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr 370 375

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp 390 395 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala 405 410 Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys 420 425 Lys Glu Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Pro Pro Val 440 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln 455 Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys 470 475 Asp Lys Thr Pro Thr Thr Lys Pro Ala Lys Ala Glu Val Glu Ser Ser 485 490 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys 505 Pro Thr Thr Ala Ser Ser Glu Thr Thr Ile Asp Val Val Gln Thr Ser 520 525 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn 535 540 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Glu Asn Asn Lys Asn 550 555 Thr Gln Glu Asn Lys Ala Lys Ser

<210> 24

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 24

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu 10 Ala Val Ala Ser Pro Ser Thr Thr Glu Lys Ala Pro Glu Ala Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro 40 45 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro 55 Lys Glu Thr Lys Glu Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr 70 75 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala 85 90 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe 105 Glu Met Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser 120 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile 135 140

Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr

150

155

Glu	Gly	Asn	Lys	Lys 165	Leu	Pro	Ile	Lys	Leu 170	Val	Ser	Tyr	Asp	Thr 175	Val
Lys	Asp	Tyr	Ala 180	Tyr	Ile	Arg	Phe	Ser 185	Val	Ser	Asn	Gly	Thr 190	Lys	Ala
Val	Lys	Ile 195	Val	Ser	Ser	Thr	His 200	Phe	Asn	Asn	Lys	Glu 205	Glu	Lys	Tyr
Asp	Tyr 210	Thr	Leu	Met	Glu	Phe 215	Ala	Gln	Pro	Ile	Tyr 220	Asn	Ser	Ala	Asp
Lys 225	Phe	Lys	Thr	Glu	Glu 230	Asp	Tyr	Lys	Ala	Glu 235	Lys	Leu	Leu	Ser	Pro 240
Tyr	Lys	Lys	Ala	Lys 245	Thr	Leu	Glu	Arg	Gln 250	Val	Tyr	Glu	Leu	Asn 255	Lys
Ile	Gln	Asp	Lys 260	Leu	Pro	Glu	Lys	Leu 265		Ala	Glu	Tyr	Lys 270		Lys
Leu	Glu	Glu 275	Thr	Lys	Lys	Ala	Leu 280	Asp	Glu	Gln	Val	Lys 285	Ser	Ala	Ile
	290		Gln			295					300				
305			Lys		310					315					320
Met	Met	Asp	Thr	Phe 325	Val	Lys	His	Pro	Ile 330	Lys	Thr	Gly	Met	Leu 335	Asn
Gly	Lys	Lys	Tyr 340	Met	Val	Met	Glu	Thr 345	Thr	Asn	Asp	Asp	Tyr 350	Trp	Lys
Asp	Phe	Met 355	Val	Glu	Gly	Gln	Arg 360	Val	Arg	Thr	Ile	Ser 365	Lys	Asp	Ala
Lys	Asn 370	Asn	Thr	Arg	Thr	11e 375		Phe	Pro	Tyr	Val 380	Glu	Gly	ГЛЗ	Thr
Leu 385	Tyr	Asp	Ala	Ile	Val 390	Lys	Val	His	Val	Lys 395	Thr	Ile	Asp	Tyr	Asp 400
Gly	Gln	Tyr	His	Val 405		Ile	Val	Asp	Lys 410		Ala	Phe	Thr	Lys 415	Ala
Asn	Ala	Asp	Lys 420		Asn	Lys	Lys	Glu 425		Gln	Asp	Asn	Ser 430	Ala	Lys
Lys	Glu	Thr 435	Thr	Pro	Ala	Thr	Pro 440		Lys	Pro	Thr	Thr 445		Pro	Val
Glu	Lys 450		Ser	Gln	Lys	Gln 455		Ser	Gln	Lys	Asp 460		Asn	Lys	Gln
Ser 465		Ser	· Val	Glu	Lys 470		Asn	Asp	Ala	Ser 475		Glu	Ser	Gly	Lys 480
Asp	Lys	Thr	Pro	Ala 485						Ala				Ser 495	
			500	)				505	i				510		Lys
Pro	Thr	Thr 515	Ala	Ser	Ser	Glu	Thr 520		Ile	Asp	Val	Val 525		Thr	Ser
	530	)				535	•				540	ı			Asn
545					550	)			Glr	Ser 555		Asn	Asn	Lys	Asn 560
Thr	Glr	Glu	ı Asn	Lys 565		Lys	s Ser								

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<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 25

Ala Glu Glu Thr Gly Gly Thr Ile Thr Glu Thr Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Ala Ala Pro 40 Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro Asn Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ser Asp Asn Asn Thr Tyr Pro Ile Leu Asn Glu Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala 90 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe 100 · 105 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser 120 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile 135 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr 150 155 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val 170 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala 185 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr 200 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp 215 220 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro 230 235 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys 250 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys 265 Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile 280 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu 295 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser 310 315 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn 330 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys 345 Asp Phe Met Val Glu Gly Glu Arg Val Arg Thr Ile Ser Lys Asp Ala 360 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr 375

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Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
                   390
                                    395
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
               405
                                   410
Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
           420
                               425
Lys Glu Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Ala Pro Val
                           440
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                        455
                                            460
Ser Pro Ser Val Glu Lys Glu Ile Asp Ala Ser Ser Glu Ser Gly Lys
                    470
                                        475
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
                                   490
Ser Thr Thr Pro Thr Lys Val Val Ser Ala Thr Gln Asn Val Ala Lys
                                505
Pro Thr Ser Ala Ser Ser Glu Thr Thr Lys Gly Val Val Gln Thr Ser
                            520
                                                525
Ala Gly Ser Ser Glu Ala Lys Asp Asn Ala Pro Leu Gln Lys Ala Asn
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Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
Thr Gln Glu Asn Lys Ala Lys Ser
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<210> 26

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 26

Ala Glu Glu Thr Gly Gly Thr Ile Thr Glu Thr Gln Pro Lys Thr Glu 10 Ala Val Ala Ser Pro Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala Pro 40 Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro 55 60 Asn Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ser Asp Asn Asn Thr 70 75 Tyr Pro Ile Leu Asn Glu Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala 90 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe 100 105 Glu Met Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser 120 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile 135 140 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr 150 155

Glu	Gly	Asp	Lys	Lys 165	Leu	Pro	Ile	Lys	Leu 170	Val	Ser	Tyr	Asp	Thr 175	Val
Lys	Asp	Tyr	Ala 180	Tyr	Ile	Arg	Phe	Ser 185		Ser	Asn	Gly	Thr 190	Lys	Ala
Val	Lys	Ile 195	Val	Ser	Ser	Thr	His 200	Phe	Asn	Asn	Lys	Glu 205	Glu	Lys	Tyr
Asp	Tyr 210	Thr	Leu	Met	Glu	Phe 215	Ala	Gln	Pro	Ile	Tyr 220	Asn	Ser	Ala	Asp
225					Glu 230			_		235					240
				245	Thr				250		_			255	_
			260		Pro			265				-	270		_
		275			Lys		280	· ·				285			
	290				Val	295					300				
305					Val 310					315					320
				325	Val				330					335	
			340		Val			345			-	_	350	_	_
		355			Gly		360					365	-		
	370				Thr	375					380		_	_	
385					Val 390					395				_	400
				405					410					415	
			420					425					430		Lys
		435	i				440					445			Val
	450					455					460				Gln
Ser 465		Ser	· Val	. Glu	Lys 470		Ile	Asp	Ala	Ser 475		Glu	Ser	Gly	Lys 480
				485	<b>;</b>				490	)				495	
			500	)				505	,				510	)	Lys
		515	5				520	)				525	•		Ser
	530	)				535	5				540	)			Asn
545	5				550	)			Glr	555		Asr	ı Asr	Lys	Asn 560
Thi	: Glr	ı Glı	ı Ası	1 Lys 565	s Ala	Lys	s Ser	•							

<210> 27 <211> 570

<212> PRT <213> Artificial Sequence <220> <223> ORF0657nH <400> 27 Met Gly Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys 10 Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu 25 Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu 40 Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys 55 Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn 85 9:0 Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile 105 Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr 120 Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro 135 140 Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu 150 155 Val Tyr Glu Gly Asp Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp 165 170 Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr 185 Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu 200 Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser 215 220 Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu 230 235 Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu 250 Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys 265 Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser 280 Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr 295 300 Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn 310 315 Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met 330 Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr 345 Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys 360 365 Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly 375

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Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp
                  390
                                   395
Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr
              405
                                  410
Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser
           420
                              425
Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser
                          440
Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn
                       455
                                         460
Lys Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser
                470
                                      475
Gly Lys Gly Val Thr Leu Ala Thr Lys Pro Thr Lys Gly Glu Val Glu
               485
                                  490
Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val
                               505
Ala Lys Pro Thr Thr Gly Ser Ser Lys Thr Thr Lys Asp Val Val Gln
                           520
                                525
Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys
                       535
                                      540
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<210> 28

<211> 654

<212> PRT

<213> Artificial Sequence

<220>

<223> SEQ ID NO: 2 modified to contain a glycine after the amino terminus methionine and a carboxyl His-Tag

<400> 28

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145					150					Glu 155					160
Gly	Thr	Gln	Gln	Phe 165	Tyr	His	Tyr	Ala	Ser 170	Ser	Val	Lys	Pro	Ala 175	Arg
Val	Ile	Phe	Thr 180	Asp	Ser	Lys	Pro	Glu 185		Glu	Leu	Gly	Leu 190		Ser
Gly	Gln	Phe 195	Trp	Arg	Lys	Phe	Glu 200		Tyr	Glu	Gly	Asp 205	Lys	Lys	Leu
Pro	Ile 210	Lys	Leu	Val	Ser	Tyr 215		Thr	Val	Lys	Asp 220		Ala	Tyr	Ile
Arg 225	Phe	Ser	Val	Ser	Asn 230		Thr	Lys	Ala	Val 235	Lys	Ile	Val	Ser	Ser 240
Thr	His	Phe	Asn	Asn 245	Lys	Glu	Glu	Lys	Tyr 250	Asp	Tyr	Thr	Leu	Met 255	
Phe	Ala	Gln	Pro 260	Ile	Tyr	Asn	Ser	Ala 265		Lys	Phe	Lys	Thr 270		Glu
Asp	Tyr	Lys 275	Ala	Glu	Lys	Leu	Leu 280	Ala	Pro	Tyr	Lys	Lys 285	Ala	Lys	Thr
Leu	Glu 290	Arg	Gln	Val	Tyr	Glu 295	Leu	Asn	Lys	Ile	Gln 300		Lys	Leu	Pro
Glu 305	Lys	Leu	Lys	Ala	Glu 310	Tyr	Lys	Lys	Lys	Leu 315		Asp	Thr	Lys	Lys 320
Ala	Leu	Asp	Glu	Gln 325	Val	Lys	Ser	Ala	Ile 330	Thr	Glu	Phe	Gln	Asn 335	Val
Gln	Pro	Thr	Asn 340	Glu	Lys	Met	Thr	Asp 345		Gln	Asp	Thr	Lys 350		Val
Val	Tyr	Glu 355	Ser	Val	Glu	Asn	Asn 360	Glu	Ser	Met	Met	Asp 365		Phe	Val
Lys	His 370	Pro	Ile	Lys	Thr	Gly 375	Met	Leu	Asn	Gly	Lys 380	Lys	Tyr	Met	Val
Met 385	Glu	Thr	Thr	Asn	Asp 390	qaA	Tyr	Trp	Lys	Asp 395		Met	Val	Glu	Gly 400
Gln	Arg	Val	Arg	Thr 405	Ile	Ser	Lys	Asp	Ala 410	Lys	Asn	Asn	Thr	Arg 415	Thr
Ile	Ile	Phe	Pro 420		Val	Glu	Gly	Lys 425	Thr	Leu	Tyr	qaA	Ala 430		Val
Lys	Val	His 435	Val	Lys	Thr	Ile	Asp 440	Tyr	Asp	Gly	Gln	Tyr 445	His		Arg
Ile	Val 450	Asp	Lys	Glu	Ala	Phe 455		Lys	Ala	Asn	Thr 460		Lys	Ser	Asn
Lys 465	Lys	Glu	Gln	Gln	Asp 470	Asn	Ser	Ala	Lys	Lys 475	Glu	Ala	Thr	Pro	Ala 480
				485					490					495	
			500					505					510		Lys
		515					520					525			Thr
	530					535					540				Lys
545					550					555					Ser 560
Lys	Thr	Thr	Lys	Asp 565	Val	Val	Gln	Thr	Ser 570		Gly	Ser	Ser	Glu 575	Ala

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Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp
Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala
                                                605
Lys Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu
                        615
                                            620
Pro Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu
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Pro Arg Lys Arg Lys Asn Leu Glu His His His His His
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<210> 29
<211> 1962
<212> DNA
<213> Artificial Sequence
<220>
<223> Full length ORF0657n + Carboxyl His-Tag
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agtccaacaa caacatctga aaaagctcca gaaactaaac cagtagctaa tgctgtctca 240
gtatctaata aagaagttga ggcccctact tctgaaacaa aagaagctaa agaagttaaa 300
gaagttaaag cccctaagga aacaaaagaa gttaaaccag cagcaaaagc cactaacaat 360
acatatecta ttttgaatea ggaaettaga gaagegatta aaaaeeetge aataaaagae 420
aaagatcata gcgcaccaaa ctctcgtcca attgattttg aaatgaaaaa gaaagatgga 480
actcaacagt tttatcatta tgcaagttct gttaaacctg ctagagttat tttcactgat 540
tcaaaaccag aaattgaatt aggattacaa tcaggtcaat tttggagaaa atttgaagtt 600
tatgaaggtg acaaaaagtt gccaattaaa ttagtatcat acgatactgt taaagattat 660
gcttacattc gcttctctgt atcaaacgga acaaaagctg ttaaaattgt tagttcaaca 720
cacttcaata acaaagaaga aaaatacgat tacacattaa tggaattcgc acaaccaatt 780
tataacagtg cagataaatt caaaactgaa gaagattata aagctgaaaa attattagcg 840
ccatataaaa aagcgaaaac actagaaaga caagtttatg aattaaataa aattcaagat 900
aaacttcctg aaaaattaaa ggctgagtac aagaagaaat tagaggatac aaagaaagct 960
ttagatgagc aagtgaaatc agctattact gaattccaaa atgtacaacc aacaaatgaa 1020
aaaatgactg atttacaaga tacaaaatat gttgtttatg aaagtgttga gaataacgaa 1080
tctatgatgg atacttttgt taaacaccct attaaaacag gtatgcttaa cggcaaaaaa 1140
tatatggtca tggaaactac taatgacgat tactggaaag atttcatggt tgaaggtcaa 1200
cgtgttagaa ctataagcaa agatgctaaa aataatacta gaacaattat tttcccatat 1260
gttgaaggta aaactctata tgatgctatc gttaaagttc acgtaaaaac gattgattat 1320
gatggacaat accatgtcag aatcgttgat aaagaagcat ttacaaaagc caataccgat 1380
aaatctaaca aaaaagaaca acaagataac tcagctaaga aggaagctac tccagctacg 1440
cctagcaaac caacaccatc acctgttgaa aaagaatcac aaaaacaaga cagccaaaaa 1500
gatgacaata aacaattacc aagtgttgaa aaagaaaatg acgcatctag tgagtcaggt 1560
aaagacaaaa cgcctgctac aaaaccaact aaaggtgaag tagaatcaag tagtacaact 1620
ccaactaagg tagtatctac gactcaaaat gttgcaaaac caacaactgc ttcatcaaaa 1680
acaacaaaag atgttgttca aacttcagca ggttctagcg aagcaaaaga tagtgctcca 1740
ttacaaaaag caaacattaa aaacacaaat gatggacaca ctcaaagcca aaacaataaa 1800
aatacacaag aaaataaagc aaaatcatta ccacaaactg gtgaagaatc aaataaagat 1860
atgacattac cattaatggc attattagct ttaagtagca tcgttgcatt cgtattacct 1920
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<211> 1737
<212> DNA
<213> Artificial Sequence
<223> ORF0657nH + Carboxyl His-Tag
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tcagtatcta ataaagaagt tgaggccct acttctgaaa caaaagaagc taaagaagtt 180
aaagaagtta aagcccctaa ggaaacaaaa gaagttaaac cagcagcaaa agccactaac 240
aatacatatc ctattttgaa tcaggaactt agagaagcga ttaaaaaaccc tgcaataaaa 300
gacaaagatc atagcgcacc aaactctcgt ccaattgatt ttgaaatgaa aaagaaagat 360
ggaactcaac agttttatca ttatgcaagt tctgttaaac ctgctagagt tattttcact 420
gattcaaaac cagaaattga attaggatta caatcaggtc aattttggag aaaatttgaa 480
gtttatgaag gtgacaaaaa gttgccaatt aaattagtat catacgatac tgttaaagat 540
tatgcttaca ttcgcttctc tgtatcaaac ggaacaaaag ctgttaaaat tgttagttca 600
acacacttca ataacaaaga agaaaaatac gattacacat taatggaatt cgcacaacca 660
atttataaca gtgcagataa attcaaaact gaagaagatt ataaagctga aaaattatta 720
gcgccatata aaaaagcgaa aacactagaa agacaagttt atgaattaaa taaaattcaa 780
gataaacttc ctgaaaaatt aaaggctgag tacaagaaga aattagagga tacaaagaaa 840
gctttagatg agcaagtgaa atcagctatt actgaattcc aaaatgtaca accaacaaat 900
gaaaaaatga ctgatttaca agatacaaaa tatgttgttt atgaaagtgt tgagaataac 960
gaatctatga tggatacttt tgttaaacac cctattaaaa caggtatgct taacggcaaa 1020
aaatatatgg tcatggaaac tactaatgac gattactgga aagatttcat ggttgaaggt 1080
caacgtgtta gaactataag caaagatgct aaaaataata ctagaacaat tattttccca 1140
tatgttgaag gtaaaactct atatgatgct atcgttaaag ttcacgtaaa aacgattgat 1200
tatgatggac aataccatgt cagaatcgtt gataaagaag catttacaaa agccaatacc 1260
gataaatcta acaaaaaga acaacaagat aactcagcta agaaggaagc tactccagct 1320
acgcctagca aaccaacacc atcacctgtt gaaaaagaat cacaaaaaca agacagccaa 1380
aaagatgaca ataaacaatt accaagtgtt gaaaaagaaa atgacgcatc tagtgagtca 1440
ggtaaagaca aaacgcctgc tacaaaacca actaaaggtg aagtagaatc aagtagtaca 1500
actccaacta aggtagtatc tacgactcaa aatgttgcaa aaccaacaac tgcttcatca 1560
aaaacaacaa aagatgttgt tcaaacttca gcaggttcta gcgaagcaaa agatagtgct 1620
ccattacaaa aagcaaacat taaaaacaca aatgatggac acactcaaag ccaaaacaat 1680
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<210> 31
<211> 1941
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes SEQ ID NO: 28 without a carboxyl His-Tag
      and is codon optimized for yeast expression
<400> 31
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ggtgttgctt ctgtcgctat ctccaccttg ttgttgttga tgtctaacgg tgaagctcaa 120
gctgctgctg aagaaactgg tggtaccaac actgaagctc aaccaaagac cgaagctgtc 180
gcttccccaa ccactacctc tgaaaaggct ccagaaacta agccagttgc taacgctgtc 240
tccgtttcta acaaggaagt cgaagctcca acctccgaaa ctaaggaagc taaggaagtt 300
aaggaagtca aggctccaaa ggaaactaag gaagtcaagc cagctgctaa ggctaccaac 360
aacacttacc caattttgaa ccaagaattg agagaagcta ttaagaaccc agctatcaag 420
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ggtacccaac aattctacca ctacgcgtcc tctgtcaagc cagctagagt tattttcacc 540
gactctaagc cagaaatcga attgggtttg caatccggtc aattctggag aaagttcgaa 600
gtctacgaag gtgacaagaa gttgccaatt aagttggttt cctacgacac cgtcaaggac 660
tacgcttaca tcagattctc cgtttctaac ggtactaagg ctgtcaagat tgtctcttcc 720
acccacttca acaacaagga agaaaagtac gactacactt tgatggaatt cgctcaacca 780
atttacaact ctgctgacaa gttcaagacc gaagaagact acaaggctga aaagttgttg 840
gctccataca agaaggctaa gactttggaa agacaagttt acgaattgaa caagatccaa 900
gacaagttgc cagaaaagtt gaaggctgaa tacaagaaga agttggaaga caccaagaag 960
gctttggacg aacaagtcaa gtccgctatc accgaattcc aaaacgttca accaactaac 1020
gaaaagatga ctgacttgca agacactaag tacgtcgtct acgaatccgt cgaaaacaac 1080
gaatccatga tggacacctt cgttaagcac ccaattaaga ctggtatgtt gaacggtaag 1140
aagtacatgg tcatggaaac cactaacgac gactactgga aggacttcat ggttgaaggt 1200
caaagagtca gaaccatctc caaggacgct aagaacaaca ctagaaccat tatcttccca 1260
tacgttgaag gtaagacttt gtacgacgct atcgtcaagg ttcacgtcaa gactattgac 1320
tacgacggtc aataccacgt tagaattgtt gacaaggaag ctttcaccaa ggctaacacc 1380
gacaagtcca acaagaagga acaacaagac aactctgcta agaaggaagc taccccagct 1440
accccatcta agccaacccc atctccagtt gaaaaggaat ctcaaaagca agactcccaa 1500
aaggacgaca acaagcaatt gccatccgtc gaaaaggaaa acgacgcgtc ttctgaatcc 1560
ggtaaggaca agactccagc taccaagcca actaagggtg aagttgaatc ttcctctact 1620
actccaacca aggttgtctc cactacccaa aacgtcgcta agccaactac cgcttcttcc 1680
aagactacca aggacgttgt ccaaacttct gctggttcct ctgaagctaa ggactctgct 1740
ccattgcaaa aggctaacat caagaacacc aacgacggtc acacccaatc ccaaaacaac 1800
aagaacactc aagaaaacaa ggctaagtct ttgccacaaa ccggtgaaga atccaacaag 1860
gacatgacct tgccattgat ggctttgttg gctttgtctt ccatcgttgc tttcgtcttg 1920
ccaagaaaga gaaagaacta a
<210> 32
<211> 1710
<212> DNA
<213> Artificial Sequence
<223> Encodes SEQ ID NO: 3 and is codon optimized for
      yeast expression
<400> 32
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gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
 tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
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 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
 ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
 aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
 tccatgatgg acacettegt taageaceca attaagactg gtatgttgaa eggtaagaag 1020
 tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1080
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gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aaggacaaga ctccagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa
<210> 33
<211> 1341
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes SEQ ID NO: 1 and is codon optimized for
      yeast expression
<400> 33
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tececaacea etacetetga aaaggeteea gaaactaage eagttgetaa egetgtetee 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat totaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1080
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gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccata a
                                                                   1341
<210> 34
<211> 1710
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes SEQ ID NO: 7 containing an amino terminus
      methionine and is codon optimized for yeast
       expression
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<400> 34
atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tececaacea etacetetga aaaggeteea gaaactaage eagttgetaa egetgtetee 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat totaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
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gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aagggtgtca ctttggctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa
                                                                   1710
<210> 35
<211> 1710
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes SEQ ID NO: 7 containing an amino terminus
      methionine and is codon optimized for yeast
      expression
<400> 35
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tececaacea etacetetga aaaggeteea gaaactaage eagttgetaa egetgtetee 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
 acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
 aaggaccact ccgctgcaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
 acccaacaat totaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
 tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
 tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
 gettacatea gatteteegt ttetaaeggt actaaggetg teaagattgt etetteeace 600
 cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
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ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
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aagggcgtca ctttggctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
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ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa
<210> 36
<211> 1710
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes SEQ ID NO: 7 containing an amino terminus
      methionine and is codon optimized for yeast
      expression
<400> 36
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tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat totaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
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gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aagggtgtta ctttggctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
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actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa
                                                                  1710
<210> 37
<211> 1710
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes SEQ ID NO: 7 containing an amino terminus
      methionine and is codon optimized for yeast
      expression
<400> 37
atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat totaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
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gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
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gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aagggcgtta ctttggctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa
<210> 38
<211> 1710
 <212> DNA
 <213> Artificial Sequence
 <223> Encodes SEQ ID NO: 7 containing an amino terminus
       methionine and is codon optimized for yeast
       expression
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<400> 38
atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tetaccacta egegteetet gteaageeag etagagttat ttteacegae 420
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gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
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tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
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gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
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ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
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aagggtgtca ctttagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
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actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa
<210> 39
<211> 1710
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes SEQ ID NO: 7 containing an amino terminus
      methionine and is codon optimized for yeast
      expression
<400> 39
atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tececaacea etacetetga aaaggeteca gaaactaage eagttgetaa egetgtetee 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat totaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
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aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
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ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa
<210> 40
<211> 1710
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes SEQ ID NO: 7 containing an amino terminus
      methionine and is codon optimized for yeast
      expression
<400> 40
atggetgaag aaactggtgg taccaacact gaagetcaac caaagacega agetgteget 60
tececaacea etacetetga aaaggeteea gaaactaage eagttgetaa egetgtetee 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat totaccacta egegteetet gteaagccag etagagttat tttcaccgae 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
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tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacqaa 960
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gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
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ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aagggtgtta ctttagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
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<210> 41
<211> 1710
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes SEQ ID NO: 7 containing an amino terminus
      methionine and is codon optimized for yeast
      expression
<400> 41
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tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
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tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
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ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
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tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1080
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gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
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ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aagggtgtta ctttggctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ctcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa
                                                                   1710
<210> 42
<211> 481
<212> PRT
<213> Artificial Sequence
<220>
<223> ORF0657nI+
Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr
                  5
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                                                         15
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Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr 25 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala 55 Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro 85 90 Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp 100 105 Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala 120 Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu 135 Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val 150 155 Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr 165 170 Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys 180 185 Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys 200 Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala 215 220 Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala 230 235 Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn 250 Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys 265 Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala 280 Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp 295 300 Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu 310 315 Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu 325 330 Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp 345 Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp 360 365 Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys 375 380 Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr 390 395 Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys 405 410 Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala 420 425 430 Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro 435 440

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Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys
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Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly
465
                    470
                                        475
Lys
<210> 43
<211> 1452
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes SEQ ID NO: 42 and is codon optimized for
      yeast expression
<400> 43
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tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat totaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
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gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aagtaaggat cc
<210> 44
<211> 605
<212> PRT
<213> ORF0657nG
<400> 44
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Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr
                                 25
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala
         35
                             40
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Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro 90 Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp 105 Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala 120 125 Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu 135 Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val 150 155 Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr 165 170 Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys 180 185 Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys 200 205 Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala 215 220 Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala 230 235 Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn 245 250 Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys 265 Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala 280 Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp 295 300 Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu 310 315 Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu 325 330 Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp 345 Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp 360 Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys 375 380 Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr 390 395 Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys 405 410 Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Asp Asn Ser Ala 420 425 Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro 440 Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys 455 Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly 470 475

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Lys Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser
                485
                                     490
Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala
            500
                                505
Lys Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr
                            520
                                                 525
Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala
                        535 ..
                                             540
Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys
                                         555
Asn Thr Gln Glu Asn Lys Ala Lys Ser Leu Pro Gln Thr Gly Glu Glu
                                     570
Ser Asn Lys Asp Met Thr Leu Pro Leu Met Ala Leu Leu Ala Leu Ser
                                 585
Ser Ile Val Ala Phe Val Leu Pro Arg Lys Arg Lys Asn
                             600
<210> 45
<211> 1818
<212> DNA
<213> Artificial Sequence
<223> Encodes SEQ ID NO: 44 containing an amino terminus
      methionine and is codon optimized for yeast
      expression
```

<400> 45

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ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1740
atgacettge cattgatgge tttgttgget ttgtetteca tegttgettt egtettgeca 1800
agaaagagaa agaactaa
<210> 46
<211> 1710
<212> DNA
<213> Artificial Sequence
<223> Encodes SEQ ID NO: 17 containing an amino terminus
      methionine and is codon optimized for yeast
<400> 46
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tecceaacca etaceactga aaaggeteca gaaactaage cagttgetaa egetgtetee 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
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aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat totaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gettacatea gatteteegt ttetaaeggt actaaggetg teaagattgt etetteeace 600
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tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
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aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
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gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
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gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa
                                                                   1710
<210> 47
 <211> 1446
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Encodes the SEQ ID NO: 17 I+ region, is codon
       optimized for yeast expression, and encodes a
       methionine initiation codon
```

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<400> 47
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tccccaacca ctaccactga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat totaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gettacatea gatteteegt ttetaaeggt actaaggetg teaagattgt etetteeace 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactetg etgacaagtt caagacegaa gaagactaca aggetgaaaa gttgttgget 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
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gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aagtaa
<210> 48
<211> 1341
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes the SEQ ID NO: 17 I region, is codon
      optimized for yeast expression, and encodes a
      methionine initiation codon
<400> 48
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tecceaacca etaceactga aaaggeteea gaaactaage cagttgetaa egetgtetee 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
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 tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
 gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
 cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
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agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
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<210> 49
<211> 1938
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes for full length ORF0657n containing SEQ ID
      NO: 17 modified to contain a glycine afer the
      amino terminus methionine and is codon optimized
      for yeast expression
<400> 49
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gctgctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttggct 180
tccccaacca ctaccactga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 240
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 300
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 360
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 420
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 480
gaacaacaat totaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 540
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 600
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 660
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 720
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 780
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 840
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 900
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 960
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 1020
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 1080
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1140
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1200
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1260
gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1320
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1380
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1440
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1500
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1560
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1620
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<210> 50

agaaagagaa agaactaa

1938

ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1680 actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1740 ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1800 aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1860 atgaccttgc cattgatggc tttgttggct ttgtcttcca tcgttgcttt cgtcttgcca 1920

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<211> 1710
<212> DNA
<213> Artificial Sequence
<223> Encodes SEQ ID NO: 20, is codon optimized for
     yeast expression, and encodes a methionine
      initiation codon
<400> 50
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tececaacea etacetetga aaaggeteea gaaactaage eagttgetaa egetgtetee 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa
                                                                   1710
<210> 51
<211> 1446
<212> DNA
<213> Artificial Sequence
<223> Encodes SEQ ID NO: 20 I+ region, is codon
      optimized for yeast expression, and encodes a
      methionine initiation codon
<400> 51
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tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
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acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat totaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
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<210> 52
<211> 1341
<212> DNA
<213> Artificial Sequence
<220>
<223> Encodes the SEQ ID NO: 20 I region, is codon
      optimized for yeast expression, and encodes a
      methionine initiation codon
<400> 52
atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tececaacea etacetetga aaaggeteea gaaactaage eagttgetaa egetgtetee 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat totaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
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cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720 ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780 aagttgccag aaaagttgaa ggctgaatac aagaagagt tggaagacac caagaaggct 840 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900 aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960 tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020 tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1080 agagtcagaa ccatctcaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140 gttgaaggta agactttgta cgacgctatc gtcaaggtc tcaacgagc taacaccgac 1260 aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320

ccatctaagc caaccccata a 1341 <210> 53 <211> 1938 <212> DNA <213> Artificial Sequence <220> <223> Encodes for full length ORF0657n containing SEQ ID NO: 20 modified to contain a glycine after the amino terminus methionine and is codon optimized for yeast expression <400> 53 atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60 ggtgttgctt ctgtcgctat ctccaccttg ttgttgttga tgtctaacgg tgaagctcaa 120 gctgctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 180 tececaacea etacetetga aaaggeteca gaaactaage cagttgetaa egetgtetee 240 gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 300 gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 360 acttacccaa ttttgaacca agaattgaga gaagctatta agaacccagc tatcaaggac 420 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 480 gaacaacaat totaccacta egegteetet gteaageeag etagagttat tttcacegae 540 tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 600 tacgaaggtg acaagaagtt gccaattaag ttggtttcct acgacaccgt caaggactac 660 gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 720 cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 780 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 840 ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 900 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 960 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 1020 aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 1080 tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1140 tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1200 agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1260 gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1320 gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1380 aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1440 ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1500 gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1560 aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1620 ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1680 actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1740 ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1800 aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1860 atgacettge cattgatgge titgttgget tigtetteea tegitgetit egictigeea 1920 agaaagagaa agaactaa 1938 <210> 54 <211> 565 <212> PRT <213> Artificial Sequence <220> <223> ORF0657nH

<400> 54 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro 40 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp 90 Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys 105 Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys 120 Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly 135 Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp 150 155 Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr 165 170 Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile 180 185 Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr 200 205 Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys 215 220 Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys 230 235 Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp 245 250 Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Leu Glu Asp 265 Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe 280 Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr 295 300 Lys Tyr Ala Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Asp 310 315 Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys 330 325 Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met 345 Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn 360 365 Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp 375 380 Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr 390 395 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp 410

Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala 420 425 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu 440 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser 455 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr 475 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Thr Thr 490 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr 505 Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser 520 Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn 535 Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu 555 Asn Lys Ala Lys Ser

<210> 55

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 55

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Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
 195 200 205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
                                         220
                      215
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
                   230
                                     235
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
              245
                                  250
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys
           260
                              265
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Pro Ala Ile
       275
                          280
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
                       295
                                          300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
                   310
                                      315
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
               325
                                  330
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
           340
                              345
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
                           360
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
                       375
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
                   390
                                      395
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
               405
                                  410
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Asp Asn Ser Ala Lys
                              425
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                           440
                                              445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                       455
                                          460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
                   470
                                      475
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
               485
                                  490
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                               505
Pro Ile Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                           520
                                               525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
                       535
                                          540
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
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 Thr Gln Glu Asn Lys Ala Lys Ser
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<220>

<sup>&</sup>lt;210> 56

<sup>&</sup>lt;211> 568

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

## <223> ORF0657nH

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Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
    420 425
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                          440
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                      455
                                         460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
                  470
                                     475
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
              485
                                 490
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Val Lys
          500
                              505
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                          520
    515
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
                      535
                                   540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
            550
                                     555
Thr Gln Glu Asn Lys Ala Lys Ser
              565
<210> 57
<211> 568
<212> PRT
<213> Artificial Sequence
<220>
<223> ORF0657nH
<221> SITE
<222> 247
<223> Unknown
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            20
                               25
Pro Val Ala Asn Ala Val Pro Val Ser Asn Lys Glu Val Glu Ala Pro
                           40
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
                       55
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
                    70
                                       75
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Thr Lys Asn Pro Glu
                                   90
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Thr Asp Phe
                               105
Glu Met Lys Lys Asn Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
                           120
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
                       135
                                           140
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
                                       155
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Glu Gly Asp Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
       165
                     170
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Ile Ser Asn Gly Thr Lys Ala
                             185
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
                      200
                                            205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
                     215
                                        220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
                 230
                                      235
Tyr Lys Lys Ala Lys Thr Xaa Glu Arg Gln Val Tyr Glu Leu Asn Lys
              245
                                  250
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys
           260
                              265
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
       275
                          280
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
                       295
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
                   310
                                      315
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
               325
                                  330
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
           340
                              345
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
                          360
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
                       375
                                          380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
                   390
                                      395
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
               405
                                  410
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                              425
                                                 430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                          440
                                             445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                       455
                                          460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
                   470
                                      475
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
                                  490
                                                     495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                               505
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                           520
                                            525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
                                         540
                       535
Leu Leu Lys Thr His Asp Gly His Thr Gln Ser Gln Asn Ile Lys Asn
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                                     555
Thr Lys Lys Asp Lys Ala Lys Ser
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<210> 58 <211> 568

<212> PRT <213> Artificial Sequence <220> <223> ORF0657nH <400> 58 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu 10 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys 25 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala 90 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe 105 Glu Met Lys Lys Glu Asn Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser 120 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile 135 140 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr 150 155 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val 165 170 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala 180 185 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr 200 : Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp 215 220 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro 230 235 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys 245 250 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys 260 265 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile 280 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu 295 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser 310 315 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn 325 330 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys 345 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala 360 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr 370 375

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Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
                  390
                           395
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                                  410
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
          420
                              425
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                          440
                                              445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                      455
                                         460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
                  470
                                      475
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
               485
                                  490
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
           500
                              505
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
      515
                          520
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
                      535
                                   540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
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                550
Thr Gln Glu Asn Lys Ala Lys Ser
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<210> 59

<211> 567

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 59

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Glu	Gly	Asp	Lys	Lys 165	Leu	Pro	Ile	Lys	Leu 170	Val	Ser	Tyr	qaA	Thr 175	Val
ГЛЗ	Asp	Tyr	Ala 180	Tyr	Ile	Arg	Phe	Ser 185	Val	Ser	Asn	Gly	Thr 190	Lys	Ala
Val	Lys	Ile 195	Val	Ser	Ser	Thr	His 200	Phe	Asn	Asn	Lys	Glu 205	Glu	Lys	Asp
	210					215					220			qaA	_
225					230					235				Pro	240
				245					250					Lys 255	
			260					265					270	Lys	
		275					280					285		Ile	
	290					295					300			Leu	
305					310					315				Ser	320
				325					330					Asn 335	_
			340					345					350	Lys	
		355					360					365		Ala	
	370					375					380			Thr	
385					390					395				Asp	400
				405					410					Ala 415	
			420					425					430		
		435	•				440					445		Val	
	450					455					460		_	Gln	
465					470	1				475					Asp 480
				485	i				490	)				Ser 495	
			500	)				505	;				510		Pro
		515	5				520	)				525			Ala
	530	)				535	•				540	l			Ile
545	•				550	)		Glr	ı Ser	555 555		Asn	Lys	. Asn	Thr 560
GIN	GIU	ı ASI	ı Lys	565		s ser									

<210> 60 <211> 576

<212> PRT <213> Artificial Sequence <220> <223> ORF0657nH <400> 60 Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu 10 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala 20 25 Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys 55 Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu 90 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala 105 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Asp Gly Thr 115 120 Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile 135 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln 150 155 Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile 165 170 Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe 185 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His 200 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala 220 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr 230 235 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu 250 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys 265 Leu Lys Ala Glu Tyr Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu 280 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro 295 300 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Ala Tyr 310 315 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His 330 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu 345 Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg 360

Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile

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Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val
                  390
                                      395
His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val
                                   410
Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys
                              425
Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro
                           440
                                              445
Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp
                       455
                                          460
Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn
                   470
                                       475
Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro
               485
                                   490
Ala Lys Ala Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val
                               505
                                                   510
Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr
                           520
                                              525
Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp
                      535
                                           540
Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His
                  550
                                      555
Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
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<210> 61

<211> 572

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 61

Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu 10 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala 25 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala 40 Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Val Lys Glu 55 Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro Ala Ala Lys Ala 70 75 Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile 85 90 Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg 100 105 Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr 120 125 His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser 135 140 Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys 150 155

Phe	Glu	Val	Tyr	Glu 165	Gly	Asp	Lys	Lys	Leu 170	Pro	Ile	Lys	Leu	Val 175	Ser
Tyr	Asp	Thr	Val 180		Asp	Tyr	Ala	Tyr 185		Arg	Phe	Ser	Val 190		Asn
Gly	Thr	Lys 195	Ala	Val	Lys	Ile	Val 200		Ser	Thr	His	Phe 205	Asn	Asn	Lys
	210					215				Phe	220				
Asn 225	Ser	Ala	Asp	Lys	Phe 230	Lys	Thr	Glu	Glu	Asp 235	Tyr	Lys	Ala	Glu	Lys 240
				245	-			_	250	Leu		_		255	-
			260					265		Glu			270		
		275					280	_	_	Ala		285			
	290					295				Gln	300				
305	THE	ASD	Leu	GIII	310	THE	гÀг	TYT	vaı	Val 315	ıyr	GIU	ser	vaı	320
Asn	Asn	Glu	Ser	Met 325		Asp	Thr	Phe	Val 330	Lys	His	Pro	Ile	Lys 335	
			340				_	345		Met			350		_
		355					360			Gln		365			
	370					375				Ile	380				
385					390					Lys 395					400
				405					410					415	
			420					425		Lys			430		
		435	<b>,</b>				440			Met		445			
	450	)				455	•				460				Asp
Asp 465		Lys	Gln	Ser	Pro 470		· Val	Glu	. Lys	Glu 475		Asp	Ala	Ser	Ser 480
Glu	Ser	Gly	/ Lys	485		Met	Pro	Val	Thr 490		Pro	Ala	Lys	Ala 495	Glu
Val	. Glu	ı Ser	Ser 500		Thr	Thr	Pro	Thr 505		: Val	Val	Ser	Thr 510		Gln
Asr	\Val	1 Ala 515		Pro	Thr	Thr	7 Ala 520		Ser	Glu	Thr	Thr 525		a Asp	Val
	530	)				535	5				540	ı			Leu
545	5				550	)				555	•		Glr	ı Ser	Gln 560
Asr	n Asr	ı Ly:	s Asr	Th:		ı Glı	ı Asr	ı Lys	570	a Lys )	Ser	•			

<210> 62 <211> 572

<212> PRT <213> Artificial Sequence <220> <223> ORF0657nH <400> 62 Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu 10 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala 25 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala 40 Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Val Lys Glu 55 Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile 85 90 Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg 105 Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr 120 His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser 135 140 Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys 150 155 Phe Glu Val Tyr Glu Gly Asp Lys Leu Pro Ile Lys Leu Val Ser 165 170 Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn 185 Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys 200 Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr 215 Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys 230 235 Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr 250 Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu 265 Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val 280 Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys 295 300 Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu 310 315 Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr 325 330 Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp 340 345 Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile 360 365 Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val 375

Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr 390 395 Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala 410 Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys Glu Gln Gln Asp 425 Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro Ser Lys Pro Thr 440 Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp 455 460 Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser 470 475 Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro Ala Lys Ala Glu 485 490 Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln 505 Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr Thr Lys Asp Val 515 520 525 Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu 535 540 Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln 545 550 555 Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser 565

<210> 63

<211> 566

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 63

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu 10 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala 20 25 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro 75 Ile Leu Asn Lys Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys 85 90 Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met 100 105 Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val 120 125 Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu 135 140 Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly 150 155

Asp	Lys	Lys	Leu	Pro 165	Ile	Lys	Leu	Val	Ser 170	Tyr	Asp	Thr	Val	Lys 175	Asp
Tyr	Ala	Tyr	Ile 180	Arg	Phe	Ser	Val	Ser 185		Gly	Thr	Lys	Ala 190		Lys
		195					200			Glu		205			
	210					215				Asn	220				
225					230					Leu 235					240
				245					250	Glu _				255	
			260					265		Tyr			270		
		275					280			Lys		285			
	290					295				Met	300				-
305	пÃ2	TÄT	vai	vaı	310	GIU	Ser	vaı	GIU	Asn 315	ASI	GIU	ser	Met	мет 320
				325					330	Gly				335	Lys
			340					345		Asp			350		
		355					360			Ser		365			
	370					375				Glu	380				
385					390					11e 395					400
				405					410					415	
			420					425		Asn			430		
		435					440					445			Lys
	450					455	,				460				Pro
Ser 465		Glu	Lys	Glu	Asn 470		Ala	Ser	Ser	Glu 475		Gly	Lys	Asp	Lys 480
Thr	Pro	Ala	Thr	Lys 485	Pro		Lys	Gly	Glu 490	Val		Ser	Ser	Ser 495	Thr
Thr	Pro	Thr	Lys 500		Val	Ser	Thr	Thr 505		Asn	Val	Ala	Lys 510		Thr
Thr	Ala	Ser 515		Glu	Thr	Thr	Lys 520		Val	. Val	Gln	Thr 525		Ala	Gly
	530	)				535	5				540	)			Lys
545	•				550	)	Gln	Ser	Glr	Asn 555		Lys	Asn	Thr	Gln 560
Glu	ı Asp	) Lys	s Ala	565		•									

<210> 64 <211> 8

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<212> PRT
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<220>
<223> His-Tag
<400> 64
Leu Glu His His His His His
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<210> 65
<211> 16
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<213> Artificial Sequence
<220>
<223> Primer
<400> 65
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ctggccgtcg ttttac
<210> 66
<211> 17
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 66
                                                                   17
caggaaacag ctatgac
<210> 67
<211> 39
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
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aaccggtttt ccatggggaa caaacagcaa aaagaattt
<210> 68
<211> 38
<212> DNA
<213> Artificial Sequence
<220>
 <223> Primer
 <400> 68
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 <210> 69
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<211> 109
<212> DNA
<213> Artificial Sequence
<220>
<223> ORF0657n oligomer
<400> 69
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ggtgttgctt ctgtcgctat ctccaccttg ttgttgttga tgtctaacg
<210> 70
<211> 110
<212> DNA
<213> Artificial Sequence
<220>
<223> ORF0657n oligomer
<400> 70
gttggggaag cgacagette ggtetttggt tgagetteag tgttggtace accagtttet 60
tcagcagcag cttgagcttc accgttagac atcaacaaca acaaggtgga
<210> 71
<211> 110
<212> DNA
<213> Artificial Sequence
<220>
<223> ORF0657n oligomer
<400> 71
agaccgaagc tgtcgcttcc ccaaccacta cctctgaaaa ggctccagaa actaagccag 60
ttgctaacgc tgtctccgtt tctaacaagg aagtcgaagc tccaacctcc
                                                                    110
<210> 72
<211> 109
<212> DNA
<213> Artificial Sequence
<220>
<223> ORF0657n oligomer
<400> 72
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Cttccttagc ttccttagtt tcggaggttg gagcttcgac ttccttgtt
<210> 73
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<212> DNA
<213> Artificial Sequence
<220>
<223> ORF0657n oligomer
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<400> 73
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<210> 74
<211> 109
<212> DNA
<213> Artificial Sequence
<220>
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<400> 74
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gaagtcgatt ggtctagagt ttggagcgga gtggtccttg tccttgata
<210> 75
<211> 102
<212> DNA
<213> Artificial Sequence
<220>
<223> ORF0657n oligomer
<400> 75
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tcgaattggg tttgcaatcc ggtcaattct ggagaaagtt cg
<210> 76
<211> 104
<212> DNA
<213> Artificial Sequence
<220>
<223> ORF0657n oligomer
<400> 76
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                                                                    104
tcaccttcgt agacttcgaa ctttctccag aattgaccgg attg
 <210> 77
 <211> 109
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> ORF0657n oligomer
 <400> 77
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                                                                     109
 gattgtctct tccacccact tcaacaacaa ggaagaaaag tacgactac
 <210> 78
 <211> 109
 <212> DNA
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<213> Artificial Sequence
<220>
<223> ORF0657n oligomer
<400> 78
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tgagcgaatt ccatcaaagt gtagtcgtac ttttcttcct tgttgttga
<210> 79
<211> 106
<212> DNA
<213> Artificial Sequence
<220>
<223> ORF0657n oligomer
<400> 79
ccgaagaaga ctacaaggct gaaaagttgt tggctccata caagaaggct aagactttgg 60
aaagacaagt ttacgaattg aacaagatcc aagacaagtt gccaga
<210> 80
<211> 109
<212> DNA
<213> Artificial Sequence
<220>
<223> ORF0657n oligomer
<400> 80
teggtgatag eggaettgae ttgttegtee aaageettet tggtgtette caacttette 60
ttgtattcag ccttcaactt ttctggcaac ttgtcttgga tcttgttca
<210> 81
<211> 109
<212> DNA
<213> Artificial Sequence
<220>
<223> ORF0657n oligomer
<400> 81
cgaacaagtc aagtccgcta tcaccgaatt ccaaaacgtt caaccaacta acgaaaagat 60
gactgacttg caagacacta agtacgtcgt ctacgaatcc gtcgaaaac
<210> 82
<211> 109
<212> DNA
<213> Artificial Sequence
<223> ORF0657n oligomer
<400> 82
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Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys Pro
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Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys Thr
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Phe	Thr	Asp	Ser 180	Lys	Pro	Glu	Ile	Glu 185	Leu	Gly	Leu	Gln	Ser 190	Gly	Gln
		195			Glu		200					205	Leu		
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465					Ser 470					475					480
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			500					505					510		Asn
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545					550					555					Thr 560
				565					570					575	Asp
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